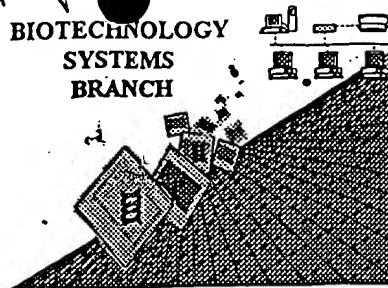


6. Bugaisky

Re-run

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/673,490

Source: OIPK

Date Processed by STIC: 7/24/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/673,490
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <u>Wrapped Nucleics</u> <u>Wrapped Aminos</u>	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <u>Invalid Line Length</u>	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <u>Misaligned Amino</u> <u>Numbering</u>	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <u>Non-ASCII</u>	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <u>Variable Length</u>	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <u>PatentIn 2.0</u> <u>"bug"</u>	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <u>Skipped Sequences</u> <u>(OLD RULES)</u>	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <u>Skipped Sequences</u> <u>(NEW RULES)</u>	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <u>Use of n's or Xaa's</u> <u>(NEW RULES)</u>	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <u>Invalid <213></u> <u>Response</u>	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <u>Use of <220></u>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <u>PatentIn 2.0</u> <u>"bug"</u>	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <u>Misuse of n</u>	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

Re-run

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,490

DATE: 07/24/2001

TIME: 10:53:52

Input Set : A:\13922.asc

Output Set: N:\CRF3\07242001\I673490.raw

Does Not Comply
Corrected Diskette Needed

5 <110> APPLICANT: The University of Queensland
9 <120> TITLE OF INVENTION: Novel omega conotoxin peptides
13 <130> FILE REFERENCE: 2338740/MJC
17 <140> CURRENT APPLICATION NUMBER: US/09/673,490
19 <141> CURRENT FILING DATE: 2000-10-16
23 <150> PRIOR APPLICATION NUMBER: PCT/AU99/00288
25 <151> PRIOR FILING DATE: 1999-04-16
29 <150> PRIOR APPLICATION NUMBER: PP2989/98
31 <151> PRIOR FILING DATE: 1998-04-16
35 <150> PRIOR APPLICATION NUMBER: PP8419/99
37 <151> PRIOR FILING DATE: 1999-02-01
41 <160> NUMBER OF SEQ ID NOS: 44
45 <170> SOFTWARE: PatentIn version 3.0

OK

pr 1-3

ERRORED SEQUENCES

229 <210> SEQ ID NO: 11
231 <211> LENGTH: 18
233 <212> TYPE: DNA
235 <213> ORGANISM: conus catus
239 <400> SEQUENCE: 11
E--> 240 agcggcaccg taggtaga 18
241 18
244 <210> SEQ ID NO: 12
246 <211> LENGTH: 382
248 <212> TYPE: DNA
250 <213> ORGANISM: conus catus
254 <220> FEATURE:
256 <221> NAME/KEY: CDS
258 <222> LOCATION: (10)..(228)
260 <400> SEQUENCE: 12
E--> 261 atcatcaaa atg aaa ctg acg tgt gtg gtg atc gtc gcc gtg ctg ctc ctg
262 51
263 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu
265 1 5 10
E--> 268 acg gcc tgt caa ctc atc aca gct aat gac tcc aga ggt acg cag aag
269 99
270 Thr Ala Cys Gln Leu Ile Thr Ala Asn Asp Ser Arg Gly Thr Gln Lys
272 15 20 25 30
E--> 275 cat cgt gcc ctg agg tcg gac acc aaa ctc tcc atg tcg act cgc tgc
276 147
277 His Arg Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys
279 35 40 45
E--> 282 aag agt aaa gga gca aaa tgt tca aag ctt atg tat gac tgc tgc agc
283 195
284 Lys Ser Lys Gly Ala Lys Cys Ser Lys Leu Met Tyr Asp Cys Cys Ser

format error - see item 1 on Error Summary Sheet

same error

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,490

DATE: 07/24/2001

TIME: 10:53:52

Input Set : A:\13922.asc

Output Set: N:\CRF3\07242001\I673490.raw

286 50 55 60
E--> 289 ggt tct tgc agc ggc acc gta ggt aga tgt ggc tgatccggcg' cttgatctcc
290 248
291 Gly Ser Cys Ser Gly Thr Val Gly Arg Cys Gly
293 65 70
E--> 296 cccttctgtg ctctatcctt ttctgctga gtcctcctta cctgagagtg gtcatgaacc
297 308
E--> 299 actcatcacc tacccctgg aggtctcaaa gaactacttg aaataaagcc gcttgcaaaa
300 368
E--> 302 aaaaaaaaaa aaaa
303 382

done

9/673,490 3

<210> 3

<211> 6

<212> PRT

<213> synthetic

see item 10 on Ena summary sheet

<400> 3

Ser Arg Leu Met Tyr Asp

1

5

This ena appears in other
sequences too

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

PSI

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/673,490

DATE: 07/24/2001

TIME: 10:53:53

Input Set : A:\13922.asc

Output Set: N:\CRF3\07242001\I673490.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:240 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:11
 L:261 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:51 SEQ:12
 L:268 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:99 SEQ:12
 L:275 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:147 SEQ:12
 L:282 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:195 SEQ:12
 L:289 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:248 SEQ:12
 L:296 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:308 SEQ:12
 L:299 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:368 SEQ:12
 L:302 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:382 SEQ:12
 L:502 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
 L:502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
 L:686 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
 L:686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
 L:713 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
 L:713 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
 L:833 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:37
 L:833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
 L:856 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
 L:856 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
 L:880 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:39
 L:880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
 L:883 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:39
 L:883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39